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DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE DNA polymerase theta.
GN POLO.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Abbas A.R., Linn S.M.;
RT "Homo sapiens polymerase (DNA-directed), theta (POLO), mRNA.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY032677; AK39635.1;
DR InterPro: IPR001410; DEAD.
DR InterPro: IPR001098; DNA_pol.
DR InterPro: IPR001650; Helicase_C.
DR Pfam: PF00270; DEAD.1.
DR Pfam: PF00476; DNA_pol_A.1.
DR Pfam: PF00271; helicase_C.1.
DR PROSITE: PS00447; DNA_POLYMERASE_A; UNKNOWN_1.
KM APP-binding: Helicase.
SQ SEQUENCE 2724 AA; 305148 MW; 30B8663614E65DC CRC64;

Query Match 18.1%; Score 75.5; DB 4; Length 2724;
Best Local Similarity 28.9%; Pred. No. 7.6;
Matches 24; Conservative 13; Mismatches 25; Indels 21; Gaps 3;

QY 20 LGDARLC-LRKTQOQKEQOILRQSEVLRFRSE-----LRKTGKGR 61
DB 86 LGERRKLCISIRKEFHMEVDVRSQCAVLPGRFTLIGLMLIGREFAMNLLRSRGR 145
QY 62 RMGSGQ--GGRGGTADTGMFLS 81
DB 146 SESGSDSFGSGGDSASPOFLS 168

RESULT 3
Q9NEB6 PRELIMINARY; PRT; 1254 AA.
AC Q9NEB6;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Kinesin-like protein.
GN L8325.12.
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-FRIEDLIN;
RA Bothe G., Pohl T., Ivens A.C., Quall M., Rajandream M.A.,
RA Barrell B.G., Pohl T., Ivens A.C., Quall M., Rajandream M.A.,
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN-FRIEDLIN;
RX MEDLINE-98146435; PubMed-9477341;
RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
RA Smith D.F.;
RT "A physical map of the Leishmania major Friedlin genome.";
RL Genome Res. 8:135-145(1998).
DR EMBL: AL157415; CAB75639.1;
DR HSP: P17119; 3KAR.
DR InterPro: IPR001752; kinesin_motor.
DR Pfam: PF00225; kinesin.1.
DR SMART: SM00129; KISC.1.
DR PROSITE: PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR PROSITE: PS50067; KINESIN_MOTOR_DOMAIN2; 1.
KM APP-binding: Coiled coil; Microtubules; Motor protein.
SQ SEQUENCE 1254 AA; 132206 MW; 79350B2F8C8B20A CRC64;

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Query Match 17.7%; Score 74; DB 5; Length 1254;
Best Local Similarity 33.9%; Pred. No. 4.9;
Matches 20; Conservative 10; Mismatches 27; Indels 2; Gaps 1;

QY 12 PIYFLSYSLGDRRLCRKTQOQKEQOILRQSEVLRFRSELTTRTKGKGRMGSGGGR 70
DB 847 YTWVLECHLGYFAAMIRHOOOORORO--RLSGTLTTSAMRAVYSSRSRSGSGGR 903

RESULT 4
Q9ILC6 PRELIMINARY; PRT; 480 AA.
AC Q9ILC6;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE ORF119, gene family 8.
OS White spot syndrome virus (WSSV).
OC Viruses; unclassified viruses.
OX NCBI_TaxID=92652;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-21342572; PubMed-11448154;
RA van Hulten M.C.W., Witteveldt J., Peters S., Kloosterboer N.,
RA van Hulten M.C.W., Witteveldt J., Peters S., Kloosterboer N.,
RA Tarchini R., Fiers M., Sandbriek H., Lankhorst R.K., Vlak J.M.;
RT "The white spot syndrome virus DNA genome sequence.";
RL Virology 286:7-22(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA van Hulten M.C.W., Witteveldt J., Peters S., Kloosterboer N.,
RA Tarchini R., Fiers M., Sandbriek H., Lankhorst R.K., Vlak J.M.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF369029; AKR77788.1;
SQ SEQUENCE 480 AA; 51006 MW; 78091EAC58E861B CRC64;

Query Match 17.5%; Score 73; DB 12; Length 480;
Best Local Similarity 27.0%; Pred. No. 2.3;
Matches 20; Conservative 19; Mismatches 35; Indels 0; Gaps 0;

QY 3 LSTHLFYFLFYFLSYSLGDRRLCRKTQOQKEQOILRQSEVLRFRSELTTRTKGKGR 62
DB 6 IATSLVFFFLFLVSTIILIDGAKTIDSPRRKRRKRRYRTSMSGIDGDTGTNGGG 65
QY 63 WGGGGRGTADTGMFLS 76
DB 66 GGGGCGGGGTNGNG 79

RESULT 5
Q8VAV1 PRELIMINARY; PRT; 486 AA.
AC Q8VAV1;
DT 01-MAR-2002 (TREMblrel. 20, Created)
DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE WSV238 (WSSV294).
OS White spot syndrome virus (WSSV).
OC Viruses; unclassified viruses.
OX NCBI_TaxID=92652;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-21548311; PubMed-11689662;
RA Yang F., He J., Lin X., Li Q., Pan D., Zhang X., Xu X.;
RT "Complete genome sequence of the shrimp white spot bacilliform
RT virus.";
RL J. Virol. 75:11811-11820(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Yang F., He J., Lin X., Li Q., Pan D., Zhang X., Xu X.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
SQ SEQUENCE FROM N.A.

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DR Pfam; PF00060; 11g\_chan; 1.  
 DR PRINTS; PRO1582; KV33CHANNEL.  
 DR ProDom; PD000500; Ion\_glu\_receptor; 1.  
 DR SMART; SM00079; PBpe; 1.  
 SO SEQUENCE 1049 AA; 116042 MW; EA1A9ABE2708E05 CRC64;

Query Match 16.9%; Score 70.5; DB 5; Length 1049;  
 Best Local Similarity 32.7%; Pred. No. 11;  
 Matches 17; Conservative 6; Mismatches 28; Indels 1; Gaps 1;

QY 28 LRKTKQOQKROQILROSEVLFRESELTAKTKGRMGCGGCGGTADTGGMF 79  
 DB 349 LRR-KPDQFRNNVQRSGTILMAVAASSTSDGYNTSASGCGGNGAGGCF 399

RESULT 8  
 09TVG7 PRELIMINARY; PRT; 1095 AA.

AC 09TVG7; (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE Iontropic glutamate receptor subunit IB precursor.  
 GN GU-RII OR GU-RII OR CG4481.  
 OS Drosophila melanogaster (fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=WT BERLIN, AND CANTON S;  
 RA Voelker M., Ienz-Boehme B., Fuchs S., Wismar J., Betz H., Schmitt B.;  
 RT "Novel glutamate receptor subunit genes of Drosophila melanogaster."  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ251886; CAB64940.1; -  
 DR HSBP; P19491; 16R2.  
 DR FLYBase; FBgn0028431; Glu-RII.  
 DR InterPro; IPR001320; Ion\_glu\_receptor.  
 DR InterPro; IPR001622; K-channel pore.  
 DR Pfam; PF00060; 11g\_chan; 1.  
 DR PRINTS; PRO1582; KV33CHANNEL.  
 DR ProDom; PD000500; Ion\_glu\_receptor; 1.  
 DR SMART; SM00079; PBpe; 1.  
 KW Receptor; Signal.  
 FT SIGNAL 1 26 POTENTIAL.  
 FT CHAIN 27 1095 IONOTROPIC GLUTAMATE RECEPTOR SUBUNIT IB.  
 SO SEQUENCE 1095 AA; 120782 MW; EDDF0316A948C32E CRC64;

Query Match 16.9%; Score 70.5; DB 5; Length 1095;  
 Best Local Similarity 32.7%; Pred. No. 11;  
 Matches 17; Conservative 6; Mismatches 28; Indels 1; Gaps 1;

QY 28 LRKTKQOQKROQILROSEVLFRESELTAKTKGRMGCGGCGGTADTGGMF 79  
 DB 342 LRR-KPDQFRNNVQRSGTILMAVAASSTSDGYNTSASGCGGNGAGGCF 392

RESULT 9  
 08RUS2 PRELIMINARY; PRT; 1150 AA.

AC 08RUS2; (TREMBlrel. 21, Created)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE Putative copia-like retrotransposon hopscotch polyprotein.  
 GN OSJNB0048022.20.  
 OS Oryza sativa (Japonica cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzaceae; Oryza.

OX NCBI\_TaxID=39947;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. NIPPONBARE;  
 RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,  
 RA Overton II L.L., Bera J.D., Tslirin T., Krol M.I., Jarrahl B.B.,  
 RA Jin S.S., Koo H., Zisman V., Hsiao J., Blunt S., Vanaken S.S.,  
 RA Utebback T.T., Feldlyum T.V., Yang Q.Q., Haas B.J., Suh B.B.,  
 RA Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M.;  
 RT "Oryza sativa chromosome 10 BAC OSJNB0048022 genomic sequence."  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AC09325; AAM1876.1; -  
 KW Polyprotein.  
 SO SEQUENCE 1150 AA; 126175 MW; 48533604BFF3D620 CRC64;

Query Match 16.6%; Score 69.5; DB 10; Length 1150;  
 Best Local Similarity 29.3%; Pred. No. 15;  
 Matches 22; Conservative 7; Mismatches 33; Indels 13; Gaps 1;

QY 16 LSYSLGDRARLCLRKTKQOQKROQILROSEVLFRESELTAKTKGRMR 62  
 DB 86 LSYSLGDRARLCLRKTKQOQKROQILROSEVLFRESELTAKTKGRMR 145

QY 63 WGGGCGGCGGTADTG 77  
 DB 146 GGGGCGGCGGNGRGG 160

RESULT 10  
 094E54 PRELIMINARY; PRT; 203 AA.

AC 094E54; (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DE Putative THY5 protein.  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzaceae; Oryza.  
 OX NCBI\_TaxID=4530;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=CV. NIPPONBARE;  
 RA Sasaki T., Matsumoto T., Yamamoto K.;  
 RT "Oryza sativa nipponebare(GA3) genomic DNA, chromosome 1, BAC  
 RT clone:OSJNB0089K24."  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF003215; BAB6258.1; -  
 DR InterPro; IPR004827; TF\_BZIP.  
 DR Pfam; PF00170; bzip; 1.  
 DR PROSITE; PS00036; BZIP\_BASIC; UNKNOWN.1.  
 SO SEQUENCE 203 AA; 21092 MW; C796B3659CD9255F CRC64;

Query Match 16.5%; Score 69; DB 10; Length 203;  
 Best Local Similarity 26.4%; Pred. No. 2.6;  
 Matches 24; Conservative 13; Mismatches 22; Indels 32; Gaps 3;

QY 19 SLGDRARLCLRKTKQOQKROQILROSEVLFRESELTAKTKGRMR 55  
 DB 105 SAGDKEONRLKRLRRNRSVAQARERKKAATMLEAKADLEIRNALEBQVSTLONENN 164

QY 56 -----TGKGRMGCGGCGGTADTG 77  
 DB 165 TLQRIILKNTTAHAGKRGCGGCGGCGGCGG 195

RESULT 11  
 09SNU6 PRELIMINARY; PRT; 296 AA.

AC 09SNU6; (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
 DE ESTs A0077435 (C12539).  
 OS Oryza sativa (Rice).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 CC Euphorbiaceae; Oryzaeae; Oryza.  
 OX NCBI\_TaxID=4530;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. NIPPONBARE;  
 RA Sasaki T., Matsumoto T., Yamamoto K.;  
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, PAC  
 RL clone: P0338C01."  
 DR EMBL: A0000391; BAA83351.1;  
 SO SEQUENCE 296 AA; 32558 MW; 3217A4F710A4FFD2 CRC64;  
 QY  
 DB 15 FLVSLGDRARLCIRKTKKOO-----KEQOILRQSFVLRSETLRKTKGRRW 63  
 169 FTSEFTS---QPCISTSPKQATELKGKAKELKKAALHQEE---KSGKGRKW 217  
 Matches 17; Conservative 14; Mismatches 12; Indels 12; Gaps 3;  
 RESULT 12  
 ID 09W1J3 PRELIMINARY; PRT; 655 AA.  
 AC 09W1J3;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE CG5543 protein (LD31556P).  
 GN CG5543.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 CC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Ananidis P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew K.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,  
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,  
 RA Buritis K.C., Busam D.A., Butler H., Cadiou E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Gerhart W.M., Glasser K.,  
 RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Heiman T.J., Wei M.-H., Ileguam C.,  
 RA Jalaal M., Kalush F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pauleb J.M.,  
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheefer F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yen R.-F., Zaveli J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster."  
 RL Science 287:2185-2195(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY;  
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,  
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,  
 RA Nuno J., Pauleb J., Pargass V., Park S., Phouanavong S., Wan K.,  
 RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: CONTAINS 5 WD REPEATS (TRP-ASP DOMAINS).  
 DR EMBL: A0003462; AAF47065.1;  
 DR EMBL: AY058624; AAL13853.1;  
 DR EMBL: FB990034908; CG5543.  
 DR InterPro: IPR001680; WD40.  
 DR Pfam: PF00400; WD40; 7.  
 DR PRINTS: PR00320; GPROTEINBRPT.  
 DR SMART: SM00320; WD40; 5.  
 DR PROSITE: PS00678; WD\_REPEATS\_1; 2.  
 DR PROSITE: PS50082; WD\_REPEATS\_2; 2.  
 DR PROSITE: PS50294; WD\_REPEATS\_REGION; 1.  
 KW Repeat; WD repeat.  
 SO SEQUENCE 655 AA; 73607 MW; 4A3EF0602E253FEC CRC64;  
 QY  
 DB 24 ARLCRKTQOQKEQOILROSEV-----LFRSE---TLRKTGKGRW----- 62  
 509 AKLCVYVTHRRKQPMKMGVGSQITTPALPLFQEKSRKTKMKRMRDVPKSRDLP 568  
 Matches 24; Conservative 13; Mismatches 19; Indels 24; Gaps 4;  
 QY 63 -WGGGGRGCTADTGMEFLS 81  
 DB 569 ITSGGGGR--VASSGGTSS 586  
 Matches 21; Conservative 11; Mismatches 14; Indels 25; Gaps 4;  
 RESULT 13  
 ID 08S5U8 PRELIMINARY; PRT; 884 AA.  
 AC 08S5U8;  
 DT 01-JUN-2002 (TREMBlrel. 21, Created)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE Putative homeodomain protein.  
 GN O0113F12.2.  
 OS Oryza sativa (japonica cultivar-group).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 CC Euphorbiaceae; Oryzaeae; Oryza.  
 OX NCBI\_TaxID=3947;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Wang R.A., Yu Y., Soderlund C., Chen W., Kim H.-R., Rambo T.,  
 RA Sasaki C., Henry D., Oates R., Simmons J.;  
 RT "Rice Genomic Sequence."  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AC104428; AAM15780.1;  
 KW Homeobox; DNA-binding; Nuclear protein.  
 SO SEQUENCE 884 AA; 94539 MW; 1F29B5DBAD0035F3 CRC64;  
 QY  
 DB Query Match 16.4%; Score 68.5; DB 10; Length 884;  
 Best Local Similarity 29.6%; Pred. No. 15;  
 Matches 21; Conservative 11; Mismatches 14; Indels 25; Gaps 4;

QY 7 LFIYLFYFEL---SYSGDARALCLRTKQOQKEQILROSEVLFSEITLRTGKGRW 63  
 DB 4 LHVILSLFPLPLFSLSTSA-FCKRRWRQR-----RRWRGRRW 45  
 QY 64 ---GGGGRG 70  
 DB 46 RHWGGGGRG 56

DB 80 KANEL--QARRDAEROGKAPGFGGSSAVSGG 112  
 Search completed: May 29, 2003, 15:20:14  
 Job time : 88 secs

## RESULT 14

ID 050357 PRELIMINARY; PRT; 165 AA.  
 AC 050357;  
 DT 01-JUN-1998 (TREMBlrel. 06, Created)  
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE CCPA & tnp genes (Fragment).  
 OS Lactobacillus casei.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;  
 OC Lactobacillaceae; Lactobacillus.  
 OX NCBI\_TaxID=1582;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 393;  
 RX MEDLINE=98012962; PubMed=9352913;  
 RA Monedero V., Gosalbes M.U., Perez-Martinez G.;  
 RT "Cataloille repression in Lactobacillus casei ATCC393 is mediated by  
 RT CCPA.";  
 RL J. Bacteriol. 179:6657-6664(1997).  
 DR EMBL; AJ003194; CAA05974.1; -.  
 FT NON TER 1  
 SQ SEQUENCE 165 AA; 16851 MW; C54BDC033EE93AC CRC64;

Query Match 16.3%; Score 68; DB 2; Length 165;  
 Best Local Similarity 35.7%; Pred. No. 2.8;  
 Matches 15; Conservative 6; Mismatches 21; Indels 0; Gaps 0;

QY 35 QKEQQLROSEVLFSEITLRTKGRWGGRGSGTADTG 76  
 DB 88 QQNQGTSENPARKVPPOTGTGTGSGNDRTGTGTGTETG 129

## RESULT 15

ID 08R1S6 PRELIMINARY; PRT; 429 AA.  
 AC 08R1S6;  
 DT 01-JUN-2002 (TREMBlrel. 21, Created)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE Hypothetical 48.0 kda protein (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=LIVER;  
 RA Strausberg R.;  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC024127; AAH24127.1; -.  
 KW Hypothetical protein.  
 FT NON TER 1  
 SQ SEQUENCE 429 AA; 47964 MW; 40ABE6564EB1BBEA CRC64;

Query Match 16.3%; Score 68; DB 11; Length 429;  
 Best Local Similarity 21.1%; Pred. No. 7.9;  
 Matches 20; Conservative 24; Mismatches 29; Indels 22; Gaps 2;

QY 3 LSTHLFIYLFYFLSLSDRRL-----CLRTKQOQKEQILR 42  
 DB 20 ISEHCFDLIFAFDEIYALGYRENVNLAQIRTFEMDSHEKVFRAVRETOERAKAMRR 79  
 QY 43 QSEVLFSEITLRTKGRWGGRGSGTADTG 77